BLAST 2 SEQUENCES

This tool produces the alignment of two given sequences using BLAST engine for local alignment. Currently only blastn and blastp programs are available. Using sequences > 150 Kb is not recommended.

Reference: Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250

Program `blastp` Matrix `0 BLOSUM62`

Parameters used in BLASTN program only:

Reward for a match: `_____` **Penalty for a mismatch:** `_____`

Open gap `11` and extension gap `1` penalties

gap x_dropoff `50` expect `1000C` word size `2` Filter `☐`

Sequence 1 Enter accession or GI `_____`

or sequence in FASTA format from: `_____` to: `_____`

```
DTYIH
```

Heavy Chain CDR1

Murine 21.6

Sequence 2 Enter accession or GI `_____`

or sequence in FASTA format from: `_____` to: `_____`

```
SYWMH
```

residues 50-54 of Seq ID NO: 15

`Align`   `Clear Input`

Comments and suggetstions to: blast-help@ncbi.nlm.nih.gov
Credits to: Tatiana Tatusov and Tom Madden

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.0.9 [May-07-1999]

Matrix `0 BLOSUM62 ▾` gap open: `11` gap extension: `1`
x_dropoff: `50` expect: `1000C` wordsize: `2` Filter ☐ `Align`

Sequence 1 lcl|seq_1 **Length** 5

Sequence 2 lcl|seq_2 **Length** 5

No siginificant similarity was found

BLAST 2 SEQUENCES

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Program [blastp ▼] Matrix [0 BLOSUM62 ▼]

Parameters used in <u>BLASTN</u> program only:

Reward for a match: [＿＿＿]　　**Penalty for a mismatch:** [＿＿＿]

Open gap [11] and extension gap [1] penalties

gap x_dropoff [50] expect [10000] word size [2] Filter [ ]

Sequence 1 Enter accession or GI [＿＿＿]

or sequence in FASTA format from: [＿＿＿] to: [＿＿＿]

    RIDPANGYTKYDPKFQG

Heavy Chain CDR2

Murine 21.6

Sequence 2 Enter accession or GI [＿＿＿]

or sequence in FASTA format from: [＿＿＿] to: [＿＿＿]

    EIDPSESNTNYNQKFKG

residues 69-85 of SEQ ID NO: 15

[Align]　[Clear Input]

Comments and suggetstions to: <u>blast-help@ncbi.nlm.nih.gov</u>
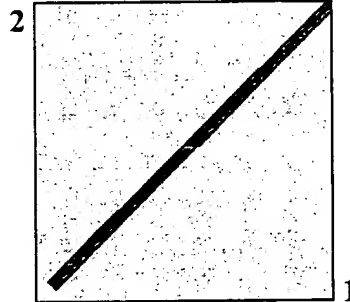*Credits to: <u>Tatiana Tatusov</u> and <u>Tom Madden</u>*

EXHIBIT
E

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.0.9 [May-07-1999]

Matrix `0 BLOSUM62 ▼` gap open: `11` gap extension: `1`
x_dropoff: `50` expect: `1000C` wordsize: `2` Filter `☐` `Align`

Sequence 1 lcl|seq_1 **Length** 17 (1 .. 17)

Sequence 2 lcl|seq_2 **Length** 17 (1 .. 17)

NOTE:The statistics (bitscore and expect value) is calculated based on the size of nr database

```
Score = 22.3 bits (46), Expect =    359
Identities = 8/16 (50%), Positives = 11/16 (68%)
```



```
Query: 2   IDPANGYTKYDPKFQG 17
           IDP+   T Y+ KF+G
Sbjct: 2   IDPSESNTNYNQKFKG 17
```

```
CPU time:     0.03 user secs.       0.02 sys. secs        0.05 total secs.
```

```
Gapped
Lambda     K        H
   0.270   0.0470    0.230
```

```
Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Hits to DB: 6
Number of Sequences: 0
Number of extensions: 1
Number of successful extensions: 1
Number of sequences better than 100000.0: 1
Number of HSP's better than 100000.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 1
length of query: 17
length of database: 90,077,593
effective HSP length: 0
effective length of query: 21
```

```
effective length of database: 90077593
effective search space: 1891629453
effective search space used: 1891629453
T: 9
A: 40
X1: 17 ( 7.3 bits)
X2: 128 (49.9 bits)
X3: 128 (49.9 bits)
S1: 29 (15.5 bits)
S2: 26 (14.5 bits)
```

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<u>Program</u> [blastp ▼] <u>Matrix</u> [0 BLOSUM62 ▼]

Parameters used in <u>BLASTN</u> program only:

Reward for a match: [   ]   **Penalty for a mismatch:** [   ]

Open gap [11] and extension gap [1] penalties

gap x_dropoff [50] expect [1000C] word size [2] <u>Filter</u> ☐

<u>Sequence 1</u> Enter accession or GI [   ]

or sequence in FASTA format from: [   ] to: [   ]

```
EGYFGNYGVYAMDY
```

Heavy Chain CDR3

21.6 Hc

<u>Sequence 2</u> Enter accession or GI [   ]

or sequence in FASTA format from: [   ] to: [   ]

```
GGYDGWDYAIDY
```

residues 118 - 129 of
SEQ ID NO: 15

[Align]   [Clear Input]

Comments and suggetstions to: <u>blast-help@ncbi.nlm.nih.gov</u>
Credits to: <u>Tatiana Tatusov</u> and <u>Tom Madden</u>

EXHIBIT
G

NCBI   *Entrez*   *BLAST 2 sequences*   *BLAST*   *Help*

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.0.9 [May-07-1999]

Matrix | 0 BLOSUM62 ▼ | gap open: | 11 | gap extension: | 1

x_dropoff: | 50 | expect: | 10000 | wordsize: | 2 | Filter | ☐ | Align

Sequence 1 lcl|seq_1 **Length** 14

Sequence 2 lcl|seq_2 **Length** 12

No siginificant similarity was found